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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/209,961DATE: 11/30/1999
TIME: 10:29:58

Input Set: I209961.RAW

<p>This Raw Listing contains the General Information Section and up to first 5 pages.</p>

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1  <110> APPLICANT: WANG, LI
2      BABIUK, LORNE A.
3      POTTER, ANDREW A.
4      WILLSON, PHILIP
5  <120> TITLE OF INVENTION: POSTWEANING MULTISYSTEM WASTING SYNDROME VIRUS FROM
6      PIGS
7  <130> FILE REFERENCE: 9000-0040
8  <140> CURRENT APPLICATION NUMBER: US/09/209,961
9  <141> CURRENT FILING DATE: 1998-12-10
10 <150> EARLIER APPLICATION NUMBER: 60/069,233
11 <151> EARLIER FILING DATE: 1997-12-11
12 <150> EARLIER APPLICATION NUMBER: 60/069,750
13 <151> EARLIER FILING DATE: 1997-12-16
14 <160> NUMBER OF SEQ ID NOS: 24
15 <170> SOFTWARE: PatentIn Ver. 2.0
16 <210> SEQ ID NO 1
17 <211> LENGTH: 1768
18 <212> TYPE: DNA
19 <213> ORGANISM: Porcine Circovirus Type II
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23      cttccgaaga cgagcgcaag aaaatacggg agctcccaat ctccctattt gattatttta 180
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26      agaaagccaa aggaactgat cagcagaata aagaatattg cagtaaagaa ggcaacttac 360
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29      tcaaaaaattt ccgcgggctg gctgaacttt tgaaagtga cgggaaaaatg caaaagcgtg 540
30      attggaaaac caatgtacac ttcattgtgg ggccacctgg gtgtggtaaa agcaaattgg 600
31      ctgctaattt tgcaaacccg gaaaccacat actggaaaacc acctaaaaac aagtgggtgg 660
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33      atgatctact gagactgtgt gatcgatata cattgactgt aaaaactaaa ggtggaactg 780
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43      cataggttag ggctgtggcc tttgttacia agttatcatc taaaataaca gcagtggagc 1380
44      ccactcccct atcacccctg gtgatggggg agcaaggcca gaattcaacc ttaacctttc 1440

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47      gcttgacagt atatccgaag gtgcgggaga ggcgggtgtt gaagatgcca tttttccttc 1620
48      tccaacggta gcggtggcgg ggggtggacga gccaggggcg gcggcgagg atctggccaa 1680
49      gatggctgcg ggggcggtgt cttcttctgc ggtaacgcct ccttggatac gtcatagctg 1740
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52 <211> LENGTH: 1759

53 <212> TYPE: DNA

54 <213> ORGANISM: Porcine Circovirus Type I

55 <400> SEQUENCE: 2

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58      gaaaaacaaa atacgggagc ttccaatctc cctttttgat tattttgttt gcggagagga 180
59      aggttttgaa gagggtagaa ctctcacct ccaggggttt gcgaattttg ctaagaagca 240
60      gacttttaac aaggtgaagt ggtatttttg tgcccgtgc cacatcgaga aagcgaagg 300
61      aaccgaccag cagaataaag aatactgcag taaagaaggc cacatactta tcgagtgtgg 360
62      agctccgcgg aaccagggga agcgcagcga cctgtctact gctgtgagta cccttttggg 420
63      gacggggtct ttggtgactg tagccgagca gttccctgta acgtatgtga gaaatttccg 480
64      cgggctggct gaacttttga aagtgcgagg gaagatgcag cagcgtgatt ggaagacagc 540
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68      actgtgtgac cggtatccat tgactgtaga gactaaaggg ggtactgttc cttttttggc 780
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71      agaacaatcc acggaggtag ccgaaggccg atttgaagca gtggaccac cctgtgcct 960
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80      ggaaaggtag gggtaggggg ttggtgccgc ctgagggggg gaggaactgg ccgatgttga 1500
81      atttgaggta gttaacattc caagatggct gcgagtatcc tccttttatg gtgagtacaa 1560
82      attctgtaga aaggcgggaa ttgaagatac cgtcttttcg gcgccatctg taacggtttc 1620
83      tgaaggcggg gtgtgccaaa tatggtcttc tccggaggat gtttccaaga tggctgcggg 1680
84      ggcgggtcct tcttctgcgg taacgcctcc ttggccacgt catcctataa aagtgaagaa 1740
85      agtgcgctgc tgtagtatt                                     1759

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86 <210> SEQ ID NO 3

87 <211> LENGTH: 314

88 <212> TYPE: PRT

89 <213> ORGANISM: Porcine Circovirus Type II

90 <400> SEQUENCE: 3

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91      Met Pro Ser Lys Lys Asn Gly Arg Ser Gly Pro Gln Pro His Lys Arg
92      1              5              10              15
93      Trp Val Phe Thr Leu Asn Asn Pro Ser Glu Asp Glu Arg Lys Lys Ile
94      20              25              30

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95      Arg Glu Leu Pro Ile Ser Leu Phe Asp Tyr Phe Ile Val Gly Glu Glu
96              35                      40                      45
97      Gly Asn Glu Glu Gly Arg Thr Pro His Leu Gln Gly Phe Ala Asn Phe
98              50                      55                      60
99      Val Lys Lys Gln Thr Phe Asn Lys Val Lys Trp Tyr Leu Gly Ala Arg
100             65                      70                      75                      80
101      Cys His Ile Glu Lys Ala Lys Gly Thr Asp Gln Gln Asn Lys Glu Tyr
102              85                      90                      95
103      Cys Ser Lys Glu Gly Asn Leu Leu Ile Glu Cys Gly Ala Pro Arg Ser
104              100                     105                     110
105      Gln Gly Gln Arg Ser Asp Leu Ser Thr Ala Val Ser Thr Leu Leu Glu
106              115                     120                     125
107      Ser Gly Ile Leu Val Thr Val Ala Glu Gln His Pro Val Thr Phe Val
108              130                     135                     140
109      Lys Asn Phe Arg Gly Leu Ala Glu Leu Leu Lys Val Ser Gly Lys Met
110             145                     150                     155                     160
111      Gln Lys Arg Asp Trp Lys Thr Asn Val His Phe Ile Val Gly Pro Pro
112              165                     170                     175
113      Gly Cys Gly Lys Ser Lys Trp Ala Ala Asn Phe Ala Asn Pro Glu Thr
114              180                     185                     190
115      Thr Tyr Trp Lys Pro Pro Lys Asn Lys Trp Trp Asp Gly Tyr His Gly
116              195                     200                     205
117      Glu Lys Val Val Val Ile Asp Asp Phe Tyr Gly Trp Leu Pro Trp Asp
118              210                     215                     220
119      Asp Leu Leu Arg Leu Cys Asp Arg Tyr Pro Leu Thr Val Lys Thr Lys
120             225                     230                     235                     240
121      Gly Gly Thr Val Pro Phe Leu Ala Arg Ser Ile Leu Ile Thr Ser Asn
122              245                     250                     255
123      Gln Thr Pro Leu Glu Trp Tyr Ser Ser Thr Ala Val Pro Ala Val Glu
124              260                     265                     270
125      Ala Leu Tyr Arg Arg Ile Thr Ser Leu Val Phe Trp Lys Asn Ala Thr
126              275                     280                     285
127      Lys Gln Ser Thr Glu Glu Gly Gly Gln Phe Val Thr Leu Ser Pro Pro
128              290                     295                     300
129      Cys Pro Glu Phe Pro Tyr Glu Ile Asn Tyr
130             305                     310
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132      <211> LENGTH: 312
133      <212> TYPE: PRT
134      <213> ORGANISM: Porcine Circovirus Type I
135      <400> SEQUENCE: 4
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138      Thr Leu Asn Asn Pro Ser Glu Glu Glu Lys Asn Lys Ile Arg Glu Leu
139              20                      25                      30
140      Pro Ile Ser Leu Phe Asp Tyr Phe Val Cys Gly Glu Glu Gly Leu Glu
141              35                      40                      45
142      Glu Gly Arg Thr Pro His Leu Gln Gly Phe Ala Asn Phe Ala Lys Lys
143              50                      55                      60
144      Gln Thr Phe Asn Lys Val Lys Trp Tyr Phe Gly Ala Arg Cys His Ile

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145      65      70      75      80
146      Glu Lys Ala Lys Gly Thr Asp Gln Gln Asn Lys Glu Tyr Cys Ser Lys
147      85      90      95
148      Glu Gly His Ile Leu Ile Glu Cys Gly Ala Pro Arg Asn Gln Gly Lys
149      100      105      110
150      Arg Ser Asp Leu Ser Thr Ala Val Ser Thr Leu Leu Glu Thr Gly Ser
151      115      120      125
152      Leu Val Thr Val Ala Glu Gln Phe Pro Val Thr Tyr Val Arg Asn Phe
153      130      135      140
154      Arg Gly Leu Ala Glu Leu Leu Lys Val Ser Gly Lys Met Gln Gln Arg
155      145      150      155      160
156      Asp Trp Lys Thr Ala Val His Val Ile Val Gly Pro Pro Gly Cys Gly
157      165      170      175
158      Lys Ser Gln Trp Ala Arg Asn Phe Ala Glu Pro Arg Asp Thr Tyr Trp
159      180      185      190
160      Lys Pro Ser Arg Asn Lys Trp Trp Asp Gly Tyr His Gly Glu Glu Val
161      195      200      205
162      Val Val Leu Asp Asp Phe Tyr Gly Trp Leu Pro Trp Asp Asp Leu Leu
163      210      215      220
164      Arg Leu Cys Asp Arg Tyr Pro Leu Thr Val Glu Thr Lys Gly Gly Thr
165      225      230      235      240
166      Val Pro Phe Leu Ala Arg Ser Ile Leu Ile Thr Ser Asn Gln Ala Pro
167      245      250      255
168      Gln Glu Trp Tyr Ser Ser Thr Ala Val Pro Ala Val Glu Ala Leu Tyr
169      260      265      270
170      Arg Arg Ile Thr Thr Leu Gln Phe Trp Lys Thr Ala Gly Glu Gln Ser
171      275      280      285
172      Thr Glu Val Pro Glu Gly Arg Phe Glu Ala Val Asp Pro Pro Cys Ala
173      290      295      300
174      Leu Phe Pro Tyr Lys Ile Asn Tyr
175      305      310
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177      <211> LENGTH: 233
178      <212> TYPE: PRT
179      <213> ORGANISM: Porcine Circovirus Type II
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183      Ser His Leu Gly Gln Ile Leu Arg Arg Arg Pro Trp Leu Val His Pro
184      20      25      30
185      Arg His Arg Tyr Arg Trp Arg Arg Lys Asn Gly Ile Phe Asn Thr Arg
186      35      40      45
187      Leu Ser Arg Thr Phe Gly Tyr Thr Val Lys Arg Thr Thr Val Thr Thr
188      50      55      60
189      Pro Ser Trp Ala Val Asp Met Met Arg Phe Lys Ile Asp Asp Phe Val
190      65      70      75      80
191      Pro Pro Gly Gly Gly Thr Asn Lys Ile Ser Ile Pro Phe Glu Tyr Tyr
192      85      90      95
193      Arg Ile Arg Lys Val Lys Val Glu Phe Trp Pro Cys Ser Pro Ile Thr
194      100      105      110

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195   Gln Gly Asp Arg Gly Val Gly Ser Thr Ala Val Ile Leu Asp Asp Asn
196           115                      120                      125
197   Phe Val Thr Lys Ala Thr Ala Leu Thr Tyr Asp Pro Tyr Val Asn Tyr
198           130                      135                      140
199   Ser Ser Arg His Thr Ile Pro Gln Pro Phe Ser Tyr His Ser Arg Tyr
200           145                      150                      155                      160
201   Phe Thr Pro Lys Pro Val Leu Asp Ser Thr Ile Asp Tyr Phe Gln Pro
202           165                      170                      175
203   Asn Asn Lys Arg Asn Gln Leu Trp Leu Arg Leu Gln Thr Ser Gly Asn
204           180                      185                      190
205   Val Asp His Val Gly Leu Gly Thr Ala Phe Glu Asn Ser Lys Tyr Asp
206           195                      200                      205
207   Gln Asp Tyr Asn Ile Arg Val Thr Met Tyr Val Gln Phe Arg Glu Phe
208           210                      215                      220
209   Asn Leu Lys Asp Pro Pro Leu Glu Pro
210           225                      230
211 <210> SEQ ID NO 6
212 <211> LENGTH: 233
213 <212> TYPE: PRT
214 <213> ORGANISM: Porcine Circovirus Type I
215 <400> SEQUENCE: 6
216   Met Thr Trp Pro Arg Arg Arg Tyr Arg Arg Arg Arg Thr Arg Pro Arg
217           1                      5                      10                      15
218   Ser His Leu Gly Asn Ile Leu Arg Arg Arg Pro Tyr Leu Ala His Pro
219           20                      25                      30
220   Ala Phe Arg Asn Arg Tyr Arg Trp Arg Arg Lys Thr Gly Ile Phe Asn
221           35                      40                      45
222   Ser Arg Leu Ser Thr Glu Phe Val Leu Thr Ile Lys Gly Gly Tyr Ser
223           50                      55                      60
224   Gln Pro Ser Trp Asn Val Asn Tyr Leu Lys Phe Asn Ile Gly Gln Phe
225           65                      70                      75                      80
226   Leu Pro Pro Ser Gly Gly Thr Asn Pro Leu Pro Leu Pro Phe Gln Tyr
227           85                      90                      95
228   Tyr Arg Ile Arg Lys Ala Lys Tyr Glu Phe Tyr Pro Arg Asp Pro Ile
229           100                     105                     110
230   Thr Ser Asn Gln Arg Gly Val Gly Ser Thr Val Val Ile Leu Asp Ala
231           115                     120                     125
232   Asn Phe Val Thr Pro Ser Thr Asn Leu Ala Tyr Asp Pro Tyr Ile Asn
233           130                     135                     140
234   Tyr Ser Ser Arg His Thr Ile Arg Gln Pro Phe Thr Tyr His Ser Arg
235           145                     150                     155                      160
236   Tyr Phe Thr Pro Lys Pro Glu Leu Asp Gln Thr Ile Asp Trp Phe His
237           165                     170                     175
238   Pro Asn Asn Lys Arg Asn Gln Leu Trp Leu His Leu Asn Thr His Thr
239           180                     185                     190
240   Asn Val Glu His Thr Gly Leu Gly Tyr Ala Leu Gln Asn Ala Ala Thr
241           195                     200                     205
242   Ala Gln Asn Tyr Val Val Arg Leu Thr Ile Tyr Val Gln Phe Arg Glu
243           210                     215                     220
244   Phe Ile Leu Lys Asp Pro Leu Asn Lys

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